

REPLACEMENT SHEET
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Figure 6

Alignment of w.t. MNT and mutant mnt-1 cDNA

MNT	*	20	*	40	*	60
ATGCCGAGTTCGGAGGTTTCATTGAAAGCTAATCGTGGAGGAGATTAATTCTCTCCTCCTCT						
ATGCCGAGTTCGGAGGTTTCATTGAAAGCTAATCGTGGAGGAGATTAATTCTCTCCTCCTCT						
mnt-1						
	*	80	*	100	*	120
GGTTTTAGTGACCCCTAAGGAGACTAGAAATGTCTCCGTCGCGCGCGAGGGGCAAAATAGC						
GGTTTTAGTGACCCCTAAGGAGACTAGAAATGTCTCCGTCGCGCGCGAGGGGCAAAATAGC						
	*	140	*	160	*	180
AATTCTACCCGATCCGCTGCGGCTGAGCGTGCCTTGGACCCCTGAGCGCTGCTCTTTACAGC						
AATTCTACCCGATCCGCTGCGGCTGAGCGTGCCTTGGACCCCTGAGCGCTGCTCTTTACAGC						
	*	200	*	220	*	240
GAGCTATGGCAGCTCTGTGCTGGTCCGCTTGTGACGGTTCCTAGACAGAGACGCGGAGTC						
GAGCTATGGCAGCTCTGTGCTGGTCCGCTTGTGACGGTTCCTAGACAGAGACGCGGAGTC						
	*	260	*	280	*	300
TTCTATTTTCCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAAACACGCGGAGTC						
TTCTATTTTCCCTCAAGGACACATCGAGCAGGTGGAGGCTTCGACGAAACACGCGGAGTC						
	*	320	*	340	*	360
CAACAGATGCCCTCTCTATGATCTCCGTCAAAGCTTCTCTGTGAGTTATTAAATGTAGAT						
CAACAGATGCCCTCTCTATGATCTCTCCGTCAAAGCTTCTCTGTGAGTTATTAAATGTAGAT						
	*	380	*	400	*	420
TTTAAAGCGAGAGGAGATACAGATGAGCTTTATGCGCAGATTAATCTCTCTCTCTGAGGCT						
TTTAAAGCGAGAGGAGATACAGATGAGCTTTATGCGCAGATTAATCTCTCTCTCTGAGGCT						
	*	440	*	460	*	480
AATCAAGACGAGAAATGCAATTGAGAAAGAGCGCCCTCTTCTCTCCACCTCGGAGGTTCCAG						
AATCAAGACGAGAAATGCAATTGAGAAAGAGCGCCCTCTTCTCTCCACCTCGGAGGTTCCAG						
	*	500	*	520	*	540
GTGCATTGCTTCTGCAAAACCTTGACTGCATCCGACACAGTACACATGGTGGATTTTCT						
GTGCATTGCTTCTGCAAAACCTTGACTGCATCCGACACAGTACACATGGTGGATTTTCT						

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* 560 * 580 * 600
GTTCTTAGGCGACATGCGGATGAATGTCTCCACCCCTCGGATATGCTCTCCACAGCCCTGCC
GTTCTTAGGCGACATGCGGATGAATGTCTCCACCCCTCGGATATGCTCTCCACAGCCCTGCC

* 620 * 640 * 660
ACTCAGAGTTAGTTCCHAGGATTTCGATGCAATGAGTGGCCATTTCAGACATATATTC
ACTCAGAGTTAGTTCCHAGGATTTCGATGCAATGAGTGGCCATTTCAGACATATATTC

* 680 * 700 * 720
CGGGGTCACCCACGGAGGCAATTGCTACAGAGTGGGTGGAGTGTCTTTGTTAGCTCCAA
CGGGGTCACCCACGGAGGCAATTGCTACAGAGTGGGTGGAGTGTCTTTGTTAGCTCCAA

* 740 * 760 * 780
AGGCTAGTTGCAGGCGATGCGTTTATATTTCTAGGGGCGAGATCCAGATTAAGAGT
AGGCTAGTTGCAGGCGATGCGTTTATATTTCTAGGGGCGAGATCCAGATTAAGAGT

* 800 * 820 * 840
GGTGTAGGCGTGCATGCCGACACAGGAAACGTGCCCTCTCTGTATATCTAGCCAT
GGTGTAGGCGTGCATGCCGACACAGGAAACGTGCCCTCTCTGTATATCTAGCCAT

* 860 * 880 * 900
AGCATGCATCTTGGAGTACGTGGCCACCGCATGGCATGCCATTTCAAGAGGGAGCTATGTT
AGCATGCATCTTGGAGTACGTGGCCACCGCATGGCATGCCATTTCAAGAGGGAGCTATGTT

* 920 * 940 * 960
ACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTTGTTCCGTTCGATCAGTAT
ACAGTCTACTACAAACCCAGGACGAGCCCATCTGAGTTTATTTGTTCCGTTCGATCAGTAT

* 980 * 1000 * 1020
ATGGAGTCTGTTAGAATAACTACTCTATTCGATGAGATTCAGATTCAGATTCAGATTCAG
ATGGAGTCTGTTAGAATAACTACTCTATTCGATGAGATTCAGATTCAGATTCAGATTCAG

* 1040 * 1060 * 1080
GAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCCGTGGGATTGAGAGTCTGATCC
GAAGAGGCTCCTGAGCAGAGGTTTACTGGCACAATCCGTGGGATTGAGAGTCTGATCC

* 1100 * 1120 * 1140
ACTAGGTGGCCAAATTCAGAGTGGAGATCCCTCAGGTCAGATGGGATGAGGCTTCAGT
ACTAGGTGGCCAAATTCAGAGTGGAGATCCCTCAGGTCAGATGGGATGAGGCTTCAGT

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* 1160 * 1180 * 1200
ATTCCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCCTCTGCT
ATTCCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTGCTCCCTCTGCT

* 1220 * 1240 * 1260
TTGAGTCCTGTTCCATGCCCTAGGCCCTAAGAGGCCCGAGTCAATATAGCACCTTCACTCT
TTGAGTCCTGTTCCATGCCCTAGGCCCTAAGAGGCCCGAGTCAATATAGCACCTTCACTCT

* 1280 * 1300 * 1320
CCTGACCTCTTCGATGCTTACCGAGAGAGGTACAACTAAGGCATACATGGACCCCTTTACCA
CCTGACCTCTTCGATGCTTACCGAGAGAGGTACAACTAAGGCATACATGGACCCCTTTACCA

* 1340 * 1360 * 1380
TCARGCCGGACTTTCAGGGTCTTGCAAGGTCAAGATACCTCGACCTTGAGGACCGAATCA
TCARGCCGGACTTTCAGGGTCTTGCAAGGTCAAGATACCTCGACCTTGAGGACCGAATCA

* 1400 * 1420 * 1440
ACTGAGAGTGTAGAGTGTGATGCTCCTGAGAAATCTGTGTCTGSCAATCTTCAGCGGAT
ACTGAGAGTGTAGAGTGTGATGCTCCTGAGAAATCTGTGTCTGSCAATCTTCAGCGGAT

* 1460 * 1480 * 1500
GATGATAGGTTGACGTGGTTTCGGGTTCTAGAAAGATATGGATCTGAGAACTGGATGCTCC
GATGATAGGTTGACGTGGTTTCGGGTTCTAGAAAGATATGGATCTGAGAACTGGATGCTCC

* 1520 * 1540 * 1560
TCAGCCAGGCATGAACTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAAGATAGAT
TCAGCCAGGCATGAACTACTTACACAGATTTGCTCTCCGGCTTTGGGACTAAGATAGAT

* 1580 * 1600 * 1620
CCATCCCATGGTCAGCGGATACCTTTTTATGACCATTCATGATGACCTTCTATGCCCTGCA
CCATCCCATGGTCAGCGGATACCTTTTTATGACCATTCATGATGACCTTCTATGCCCTGCA

* 1640 * 1660 * 1680
AAGAGAAATCTTGAGTGATTCAGAAAGGCAAGTTGGATTATCTTGCTAACCACTGGCAGATG
AAGAGAAATCTTGAGTGATTCAGAAAGGCAAGTTGGATTATCTTGCTAACCACTGGCAGATG

* 1700 * 1720 * 1740
ATTACACTCTGGTCTCTCCCTGAGTTACATGAATCTCCTAAGGTACCTGCGGCACTGAT
ATTACACTCTGGTCTCTCCCTGAGTTACATGAATCTCCTAAGGTACCTGCGGCACTGAT

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* 1760 * 1780 * 1800
GCGTCTCTCCAGGGCCGATGCATGTTAATACAGCGAATATCCTGTTCTTAATGGTCTA
GCGTCTCTCCAGGGCCGATGCATGTTAATACAGCGAATATCCTGTTCTTAATGGTCTA

* 1820 * 1840 * 1860
TCGACTGAGAAAGCTGGTGGTAACTGGCCAAATACGTCCACGTGCTTTGAATATTATAGAG
TCGACTGAGAAAGCTGGTGGTAACTGGCCAAATACGTCCACGTGCTTTGAATATTATAGAG

* 1880 * 1900 * 1920
GAAGTGGTCAATGCTCAGGCGAAGCTCAGGCTAGGGAGCAAGTAACAAACACACCCCTTC
GAAGTGGTCAATGCTCAGGCGAAGCTCAGGCTAGGGAGCAAGTAACAAACACACCCCTTC

* 1940 * 1960 * 1980
ACGATACAGAGGAGACAGCAAGTCAAGAGAGGGGAACTGCAGGCTCTTTGGCATTCCT
ACGATACAGAGGAGACAGCAAGTCAAGAGAGGGGAACTGCAGGCTCTTTGGCATTCCT

* 2000 * 2020 * 2040
CTGACCAACACATGATGGGACAGACTCAACCATGTCTCAGAGAAACAACTTGAATGAT
CTGACCAACACATGATGGGACAGACTCAACCATGTCTCAGAGAAACAACTTGAATGAT

* 2060 * 2080 * 2100
CCTCCCCCGCTTACACACATACCAACACCCAAAGCTTCACCAACCTTTCACATCACTCAAA
CCTCCCCCGCTTACACACATAGCATCAACAAAGGTTCAAGGACCTTTCAGATCACTCAAA

* 2120 * 2140 * 2160
GGGTCAAAATCAACAAACGATCATCGTGAACAGGGAGACCAATCCAGACTAATATTCCT
GGGTCAAAATCAACAAACGATCATCGTGAACAGGGAGACCAATCCAGACTAATATTCCT

* 2180 * 2200 * 2220
CATCCGAGGGATGCTCAACCGAATACCAACTCAAGTAGGAGTTGCACAAAGGTTCAACAG
CATCCGAGGGATGCTCAACCGAATACCAACTCAAGTAGGAGTTGCACAAAGGTTCAACAG

* 2240 * 2260 * 2280
CAGGGAAATGCHCTTGGCCGTTCACTGGATCTTTCAAGTTCCAAACATATGAGGAGTTA
CAGGGAAATGCHCTTGGCCGTTCACTGGATCTTTCAAGTTCCAAACATATGAGGAGTTA

* 2300 * 2320 * 2340
GTCCGTGAGCTGGACAGGCTGTTTGAGTTCAATCGAGAGTTGATGGCTCCTAAGAAACAT
GTCCGTGAGCTGGACAGGCTGTTTGAGTTCAATCGAGAGTTGATGGCTCCTAAGAAACAT

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* 2360 * 2380 * 2400
TGGTTGATAGTTTACACAGATGAAGAGATTGATATGATGCTTGTGGTGACGATCCTTGG
TGGTTGATAGTTTACACAGATGAAGAGATTGATATGATGCTTGTGGTGACGATCCTTGG

* 2420 * 2440 * 2460
CAGGAGTTTGTTCATGCTTCCCAAAATCTTCATATACACGAAGAGGAAGTGAGGAAAG
CAGGAGTTTGTTCATGCTTCCCAAAATCTTCATATACACGAAGAGGAAGTGAGGAAAG

* 2480 * 2500 * 2520
ATGAACCCGGGGACTTTAAGCTGTAGGACCGAGGAGGAGCAGTTGTTGGGGAGGGATCA
ATGAACCCGGGGACTTTAAGCTGTAGGACCGAGGAGGAGCAGTTGTTGGGGAGGGATCA

* 2540 * 2560 * 2580
GATGCAAAGGACGGCCAGTCTGCATCAATCCCTTCATTGTCCAGCGCTGGGAGCTCTTAA
GATGCAAAGGACGGCCAGTCTGCATCAATCCCTTCATTGTCCAGCGCTGGGAGCTCTTAA

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SEQ ID NO: 5

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Figure 7

Alignment of w.t. MNT and mutant mnt-1 protein

MNT	*	20	*	40	*	60
MASSEVSMKGNRGGDNFSSSGFSDPKETRIIVSVAGEGOKSHSTRSAAAEALDPEAALYR						
MASSEVSMKGNRGGDNFSSSGFSDPKETRIIVSVAGEGOKSHSTRSAAAEALDPEAALYR						
mnt-1						
	*	80	*	100	*	120
ELWHACAGPLVIVPRQDDRVFYTFQGHIEQVEASTHQAREQQMPLDYLP SKLLCRVIVHD						
ELWHACAGPLVIVPRQDDRVFYTFQGHIEQVEASTHQAREQQMPLDYLP SKLLCRVIVHD						
	*	140	*	160	*	180
LKAEKDTAEVYAOITLPEANODENAIKKEAPIPPEPRPQVHSFCSTGLASDTSTHGGEE						
LKROIQKFMERDLETIRLIKTRMQLRKKRLERHGRSREERSAKP-----						
	*	200	*	220	*	240
VLRNADPCLEPLWSEDPPTQRIYARDIHANETRFTHLTCQPKRIHLCQSGWEVTVLKL						

	*	260	*	280	*	300
RYAGDRIEFLGENCEIRVGVHRAHQGNVLSSTSSHSMLGCTATVHATSTGDAE						

	*	320	*	340	*	360
LYYKHLSTFSEFAPEDQYNEVYNNYKIGMRKQRIEGERAPEQRETFCTIVGTERSON						

	*	380	*	400	*	420
TRWPKSGIRFLQWDETSFEPREDVSNHVERAAGNPAISPYMDRDKERENTAGEE						

	*	440	*	460	*	480
PDSSMLTHGGTTCANMDLPAAGLSRVLOGGHYSTERTKHTERYECDAPENSVYQSSAN						

	*	500	*	520	*	540
DDKYDVVSGSRRYCSENWMSARHEPTYTDLTSCFGTNIDPSHCORIPFYDHSSSPFMR						

	*	560	*	580	*	600
KRLSDSEGGKDYLANOWMIHSGLSIKLHESPKYPAATDASLOGECHVKYSEYFVLNGE						

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620 640 660
STENAGGNNPFRPRALNYZEEVVNAOAOAOAREQVAKOPFTIOEETAKSREGNCRLEGTE

680 700 720
LTNNMNGADSTMSQNNLNDAGLTQFASPIVODLSDOSKGSKSTNDREOCGRPEQND

740 760 780
NPKOAOULNFSRSQKVIKOSVAPERSVULSKCQVPESTVAPLDRFTLNOFANAKKE

800 820 840
NDAVVLDEENDMMGVGDOPWOEECCVRIKTEVKEEYKONPFTUSCRFREEAVYGE

SEQ ID NO: 3

DAKAKSRSNPELSECKE

SEQ ID NO: 6

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Figure 8

Alignment of MNT and BnARF2 cDNA

MNT * 20 * 40 * 60
ATGGCGAGTTCCGGAGGTTTCTATGAAGCCTATTCGTGGA---CCAGTTAACTTCTCTCTCC
ATGGCGAGTTCCGGAGGTTTCTATGAAGCCTATTCGTGGAAGGAGAACTTCTCTCTCC

BnARF2

* 80 * 100 * 120
TCTGGTTTATGTGACCCAAAGGAGACCTGTAAGGACGCTCGCCGGCGAGGGGCAATAAA
CTCTGGTTTATGTGACCC-----GAC-----CTCCCGGCGAGGGGCGTCAAA

* 140 * 160 * 180
AGTAATTTCTACCCGATCCGCTGCGGCTGAGCGTGGCTTTCGACCCCTGAGGCTGCTCTTTAC
ACTCAGTCTTAACCGATCTGTGGCTGCGAGCGGCTTTCGACCCCGTAAGCTGCTCTTTAC

* 200 * 220 * 240
AGGAGCCTATGGGCACGCTTGTGCTGGTCCGCTTGTGACGTTTCTAGACAGAGCGACCGA
CTGTAGCTGTGGGCACGCTTGTGCTGGTCCGCTTGTGACAGTCCCTCGACAGATGACCGA

* 260 * 280 * 300
GTCTTCTATTTTCTCAATGACACATCGAGCAGGTGGAGGCTTCGACGATCGAGGCTGCA
GTCTTCTATTTTCTCAATGACACATCGAGCAGGTGGAGGCTTCGACAAATCAAGCTGCT

* 320 * 340 * 360
GACACACAGATGCCCTCTCTATGATCTTCCGCTCAAGCTTCTTGTCCGAGTTATTAAAGTA
GAACAGCAGATGCCCTCTCTATGATCTTCCGCTCAAGCTTGTTCGAGTCTTGTTCGATTAAGTT

* 380 * 400 * 420
GATTTAAGGCAGAGGCAGATACAGATGAAGTTATGCCGAGATTACICTTCTTCCCTGAG
GATTTAAGGCAGAGGCAGATACAGATGAAGTTATGCCGAGATTACICTTCTTCCCTGAG

* 440 * 460 * 480
GCTAATCAAGACGAGAATTCATTTGAGAAAGAGCGGCTCTTCCCTCCAGCTCCGAGGTTT
CTGTTCAGACGAGAATTCATTTGAGAAAGAGCGGCTCTTCCCTCCAGCTCCGAGGTTT

* 500 * 520 * 540
CAGGTCCTATTCGTTCTGCAAAACCTTGACTGCATCCGACACAGTACACATGGTGGATT
CAGGTCCTATTCGTTCTGCAAAACCTTGACTGCATCCGACACAGTACACATGGTGGATT

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* 560 * 580 * 600
 TCTGTTCTTAGGCGACATGCGGATGATGTCTCCCACCTCTGGATATGTCTCGACAGGCT
 TCTGTTCTTAGGCGGACATGCGGATGATGTCTCCCACCTCTGGATATGTCTCGACAGGCT

* 620 * 640 * 660
 CCAGCTCAAGAGTTAGTTGCAATGATGCGATGCAATGAGTGGCGATTGAGACATATG
 CCTACTCAGGAGTTAGTTGCAATGATGCGATGCAATGAGTGGCGATTGAGACATATG

* 680 * 700 * 720
 TTCCGGGGTCAACCCACGAGGCCATTGCTTCAGAGTGGGTGGAGTGTGTTGTTAGCTCC
 TTCCGGGGTCAACCCACGAGGCCATTGCTTCAGAGTGGGTGGAGTGTGTTGTTAGCTCC

* 740 * 760 * 780
 ATAGGCCCTGTTGAGGCCGATGCCCTTTATATTTCTAGGGGGCGAGATGGAGATTTAGG
 ATAGGCCCTGTTGAGGCCGATGCCCTTTATATTTCTAGGGGGCGAGATGGAGATTTAGG

* 800 * 820 * 840
 GTTGGGTGAAGGCCGTGCCATGCCGCAATGAGGAAATGAGGCCCTCTTCTCTTATATCTAGC
 GTTGGGTGAAGGCCGTGCCATGCCGCAATGAGGAAATGAGGCCCTCTTCTCTTATATCTAGC

* 860 * 880 * 900
 CATAGCATGCAATCTTGGAGTATGAGGCCATGGCATGGCATGGCATTTTCAACAGGAGATATG
 CATAGCATGCAATCTTGGAGTATGAGGCCATGGCATGGCATGGCATTTTCAACAGGAGATATG

* 920 * 940 * 960
 TTTACAGTCTACTATATACCAGGRCAGGCGCATCTCAGTTTATTTCTTCCGTTCGATCAG
 TTTACAGTCTACTATATACCAGGRCAGGCGCATCTCAGTTTATTTCTTCCGTTCGATCAG

* 980 * 1000 * 1020
 TATATGGAGTCTTATATGATTAATCTACTCTATTGGCATGAGATTCAAAAGAGATTTGAA
 TATATGGAGTCTTATATGATTAATCTACTCTATTGGCATGAGATTCAAAAGAGATTTGAA

* 1040 * 1060 * 1080
 GGCGAAGAGGCTCGTGGAGAGAGGTTTACTGGCACAATCGTTGGGATTCAGAGCTCTGAT
 GGCGAAGAGGCTCGTGGAGAGAGGTTTACTGGCACAATCGTTGGGATTCAGAGCTCTGAT

* 1100 * 1120 * 1140
 CCTACTAGGTGGGCAAAATCAATGAGGATCCCTCAGGTTGAGATGGGATGAGATCTCT
 CCTACTAGGTGGGCAAAATCAATGAGGATCCCTCAGGTTGAGATGGGATGAGATCTCT

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* 1160 * 1180 * 1200
AGTATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTCCICCCCI
AGTATTCCTCGACCTGATAGAGTATCTCCGTGGAAAGTAGAGCCAGCTCTTCTCICCI

* 1220 * 1240 * 1260
GCCTTGAGTCCCTGTACCAATGCCTAGGCCCTAAGAGGCCAGATCTAATAGGACCTTCA
GCCTTGAGTCCCTGTACCAATGCCTAGGCCCTAAGAGGCCAGATCTAATAGGACCTTCTCA

* 1280 * 1300 * 1320
TCTCCGACCTCTTCGATGCTTAGCAGAGAGGGTACAACTAAGGCCAATCATGGACCTTTA
TCTCCGACCTCTTCGATGCTTAGCAGAGAGGGTACAACTAAGGCCAATCATGGACCTTTA

* 1340 * 1360 * 1380
CCGCGCAGTGGACTTTCAGGGGCTTGCAAGGTCAGGAAATCTCGACCTTGAGGACGAA
CCGCGCAGTGGACTTTCAGGGGCTTGCAAGGTCAGGAAATCTCGACCTTGAGGACGAA

* 1400 * 1420 * 1440
CATCTGAGAGTGTAGATCTGATGCTCCCTGCAATTTCTTTGTCTGGCATTCTTCAGCC
CATCTGAGAGTGTAGATCTGATGCTCCCTGCAATTTCTTTGTCTGGCATTCTTCAGCT

* 1460 * 1480 * 1500
GATGATGATAGGTTGAGCTGCTTTCGGCTTCTAGAGGATTCATCTGAGAACTGCAATG
GATGATGATAGGTTGAGCTGCTTTCGGCTTCTAGAGGATTCATCTGAGAACTGCAATG

* 1520 * 1540 * 1560
TCCICAGCCAGGCATGACCTACTTTCACAGATTTCCTCCGCTTTGGGACTAACATG
TCCICAGCTAGGCATGACCTACTTTCACAGATTTCCTCCGCTTTGGGACTAACATG

* 1580 * 1600 * 1620
GATCCATCCCATCTCTCAGGATACCTTTTATGACCGTT---CATCATCACCTTCATG
GATCCATCCCATCTCTCAGGATACCTTTTATGACCGTTTATCATCATCACCTTCATG

* 1640 * 1660 * 1680
CCTGCAAGAGAGATCTGAGTGAATTCAGAAAGCAAGTTGATATCTTGCCTAACCACTGG
CCTGCAAGAGAGATCTGAGTGAATTCAGAAAGCAAGTTGATATCTTGCCTAACCACTGG

* 1700 * 1720 * 1740
GAGATGATACACTCTGCTCTTCCCTGAGGTTACATGAACTCCCTAGCTACCTGGACCA
---ATGATGCACTCAGGCTTCCCTGAGGTTACATGAACTCCCTAGGTTCCCTGGACCA

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* 1760 * 1780 * 1800
ACTGATGCCCTCTCTCCAGGGCCGATSCAATGTTAAATACGCCAATATCTCTTCTTAAT
TCTGATGCCCTCTCTCCAGGGATAGSCAATGCCAATTACGCCAATATCTCTTCTTAAAT

* 1820 * 1840 * 1860
GGTCTATCGACTGAGATGCTGGTGGTAACTGGCCAAATACGTCCACGTGCTTGAATTA
GAGTGAAGACTGAGATGCTGGTGGTAACTGGCCAAATACGTCCACGTGCTTGAATTA

* 1880 * 1900 * 1920
TATGAGGAAGTGGTGAATGCTCAGGCGAAGCTCAGGCTAGCGAGCACTTACAAATACAT
TTTGAAGAGCGGT-----TCAT-----GCTCAGGCTAGAGAGCATCTGACAAATGCT

* 1940 * 1960 * 1980
CCCTTCA--CGATACAGAGGGAGACAGCRAAGTCAAGAGAGAGGGAACTGCGAGGCTTTTG
CC-TCCGCTCC-TACAGAGGGAGGACAGCRAAGCAGAGAGAGGGAACTGCGAGGCTTTTG

* 2000 * 2020 * 2040
GCATTCCCTCTGTCGAACACATGAATGGGACAGACTCAACGATGCTCTCAGAGAACACAT
GCATTCCCTCTGTCGAACACATGAATGGGACAGACTCAACGATGCTCTCAGAGAACACAT

* 2060 * 2080 * 2100
TGAATGATGCTGCGGGGGCTTACACAGATAGCATCACCAAGGGTTCAGGAGCTTCTGAT
TGAATGATGCTGCGGGGGCTTACACAGATAGCATCACCAAGGGTTCAGGAGCTTCTGAT

* 2120 * 2140 * 2160
AGTCAAAGGGGTCAAATCCAAACGATCATCGTGAACAGGGAGACCATTCAGAGCT
AGTCAAAGGGGTCAAATCCAAACGATCATCGTGAACAGGGAGACCATTCAGAGCT

* 2180 * 2200 * 2220
ATATTCCTCATCCGAGGATGCTCAACCAAAAGCACTCAAGTGGAGCTTCAACAAAGG
GTAATCCCATCCGAGGATGCTCAACCAAAAGCACTCAAGTGGAGCTTCAACAAAGG

* 2240 * 2260 * 2280
TTCAACAGCAGGGGATTTGCACTTGGCCGTTCAGTGGATCTTCAAAAGTTCCAAACTATG
TTCAACAGCAGGGGATTTGCACTTGGCCGTTCAGTGGATCTTCAAAAGTTCCAAACTATG

* 2300 * 2320 * 2340
AGGAGTTATCTGCTGAGCTGGACAGGCTCTTTCAGTTCAATCCGAGGTTGATGCTCTTA
AGGAGTTATCTGCTGAGTTGGATAGGCTCTTTCAGTTCAATCCGAGGTTGATGCTCTTA

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* 2360 * 2380 * 2400
 AGAAGATTGGTIGATAGTTTACACAGATGAAGAGATGATATGATGCTTGTGGTACCG
 AGAAGATTGGTIGATAGTTTACACAGATGAAGAGATGATATGATGCTTGTGGTACCG

* 2420 * 2440 * 2460
 ATCCTTGGCAGGAGTTTTGTTGCATGGTTCCGAAATCTTCATATACACGAAAGAGGAGG
 ATCCTTGGCAGGAGTTTTGTTGCATGGTTCCGAAATCTTCATATACACGAAAGAGGAGG

* 2480 * 2500 * 2520
 TCAGGARGATGACCCCGGGSACTTTAGCTGTAGGAGCGAGGAAGAGCAGTTGTTGGGG
 TCAGGARGATGACCCCGGGSACTTTAGCTGTAGGAGCGAGGAAGAGCAGTTGTTGGGG

* 2540 * 2560 * 2580
 AAGGATCAGATGCAAGGACGCGAAGTCTGCATCAATTCCTTCATTGTCCAGCGGCTGCGA
 AAGGATCAGATGCAAGGACGCGAAGTCTGCATCAATTCCTTCATTGTCCAGCGGCTGCGA

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ACTCTTAA
 ACTCTTAA

SEQ ID NO: 9

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Figure 9

Alignment of MNT, BnARF2, OsARF2 proteins

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      *           20           *           40           *
MNTwt : MASSEVSMKGNRG-CDFSSSGFSDEKETRNVSTAGEGQKSNSTRSAATERALDL
BnARF2 : MASSEVSMKGNRGRCDFSSAGYSDE-----TAGGAQKTQSNRSVAAERVVDP
OsARF2 : -----GDD

      60           *           80           *           100           *
MNTwt : EARLYRELWHACAGPLVTVPQDDRVFYFPQGHILEQVEASTNQAEQQMPLYDLF
BnARF2 : EARLYRELWHACAGPLVTVPQDDRVFYFPQGHILEQVEASTNQAEQQMPLYDLF
OsARF2 : ---LYDELWHACAGPLVTVPQDGLVFYFPQGHILEQVEASNQVAQSQMRLYDLF

      120           *           140           *           160
MNTwt : SKLLCRVLIIVELKAEADTDEVYAAQITLLPEARNQDENATEKEAPLDDP---PRFQVH
BnARF2 : SKLLCRVLIIVDLKAEADTDEVYAAQITLLPEPVQDLISILKEAPEPPD---PRFQVH
OsARF2 : SKLLCRVLIIVELKAEQDTDEVYAAQITLLPEDEQNEQMAVEKTTTSGQVQAEPFPR

      *           180           *           200           *           220
MNTwt : SFCKTLTASDTSTHGGFSVLRHHADECLPPLDLSKQDPTQELVAKDLHANEWLFR
BnARF2 : SFCKTLTASDTSTHGGFSVLRHHADECLPPLDLSKQDPTQELVAKDLHASLWNFR
OsARF2 : SFCKTLTASDTSTHGGFSVLRHHADECLPPLDLSKQDPTQELVAKDLHSMQWFR

      *           240           *           260           *
MNTwt : HIFRGQPPRHLLQSGWSVVFVSSKRLVAGDAFIFLRGENGELRVGVRRMRQGGNV
BnARF2 : HIFRGQPPRHLLQSGWSVVFVSSKRLVAGDAFIFLRGENGELRVGVRRMRQGGNV
OsARF2 : HIFRGQPPRHLLQSGWSVVFVSSKRLVAGDAFIFLRGENGELRVGVRRMRQLSNV

      280           *           300           *           320           *
MNTwt : PSSVTSSEHMLGLVLAFAWHAISTETMTFTVYYKPRTSPSEFIPTFDQYMESVKNN
BnARF2 : PSSVTSSEHMLGLVLAFAWHAISTETMTFTVYYKPRTSPSEFIPTFDQYTESVKNN
OsARF2 : PSSVTSSEHMLGLVLAFAWHAISTETMTFTVYYKPRTSPSEFIPTFDQYMESVKNN

      340           *           360           *           380
MNTwt : YSIGMRFMRFEGEEAPEQRFTGTITVGTIESDPTKWPKSKWRSCLKVRWDETSSIP
BnARF2 : YSIGMRFMRFEGEEAPEQRFTGTITVGTIESDPTKWPKSKWRSCLKVRWDETSSIP
OsARF2 : YSVGMRFMRFEGERAPEQRFTGTITVGTIESDPTKWPKSKWRSCLKVRWDEPSTIP

      *           400           *           420           *           440
MNTwt : RPDVSPKYLEPALAPPALSPVDMRPPKRPNSLIAPSSPDSSMLTRECTTKAMND
BnARF2 : RPDVSPKYLEPALAPPALSPVDMRPPKRPNSLIAPSSPDSSMLTRECTTKAMND
OsARF2 : RPDVSPKYLEPALAPPALSPVDMRPPKRPNSLIAPSSPDSSMLTRECTTKAMND

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* 460 * 480 *
 MNTwt : PLPA--SELSEVLQGEYSFLRKHVESVECDAPENS-VVWQSSADDDKVDVVS
 BnARF2: PLPA--SELSEVLQGEYPTLRKHVESVECDAPENS-VVWQSSADDDKVDVISA
 OsARF2: DAQFORSONSTVLOGQEQMLRSLNLSNDSNDSVTAKKPMANSPSPNAAKAHPLTF

500 * 520 * 540 *
 MNTwt : SRRYGSERFMSSARHEPTVDDLSCGCTNIDPSHGQRIFHYDH-SSSPSMPA-RK
 BnARF2: SRRY--ENMTSSGNHGPTCDLSCGCTNIEPPHGHQIDFYDRLSSDPSVA-RK
 OsARF2: QQRFPMDNMQLSRRETDFKDVRSQ-SQSFGDSPAFFMNFDE--ADNRLTSFNN

560 * 580 * 600
 MNTwt : ILSDSSEKFDYLANQKQMHSGLSLKLHESPKVPARTDASLOERCHVYSEYVVL
 BnARF2: ILSDDQEKFEYLANQVMMHSGLSLKLHESPKVPARTDASFOEIGIPNYGEYALP
 OsARF2: QFQDQ--SARHFSDPYYYV-----SPOPSLTVESSTQMTDSK--ELHFW

* 620 * 640 * 660
 MNTwt : NGLSTENAGSHKFINPRALNYYEVVNAQADAQR-EG-VTKQFTTICF-ETAY
 BnARF2: KAVTTEHAGSHKFINPRALNYYEVVNAQADAQR-EG-VTKQFTTICF-ETAY
 OsARF2: NGQST--VYGNRDRDQNFREFEQNSSWLNSFARFQPRVIRPHASTAFVELEN

* 680 * 700 *
 MNTwt : SRETHCRNLCGIP-LTRM--NFTSTMSQHN--LNDAGLTQIASPKVQDLSLC
 BnARF2: PROTHCRNLCGIP-LTRM--NFTSTMSQHN--LNDAGLTQIASPKVQDLSLC
 OsARF2: TEGSGFKIEGFKVDITRAPNHLSSPLAATHEPMLQTESSENQLOFVQDCIPEV

720 * 740 * 760 *
 MNTwt : SKGSKSTNDHREQGRPTQNNPHKDAQTKTN--SSRSCTKVHKQGLALGRSVDI
 BnARF2: SKGSKSTNDHREQGRPTQNNPHKDAQTKTN--SSRSCTKVHKQGLALGRSVDI
 OsARF2: SVSTAGTATENEKSG--QQAQSSKDVQSKQVASTESCTKVHKQGLALGRSVDI

780 * 800 * 820
 MNTwt : SKFQHYEELVAELDRLEFNGELMAPKKDWLIYYTDEENDMLLVGDDPWQEFCCM
 BnARF2: SKFQHYEELVAELDRLEFNGELMAPKKDWLIYYTDEENDMLLVGDDPWQEFCCM
 OsARF2: SKFSHYDELKAEELDKMEFEDGELVSSKNQVLYTDEENDMLLVGDDPWQEFCCM

* 840 * 860 *
 MNTwt : VRKIFLYIKKEEVKQNNPGTILSRSEEEAGVCEGSDAKDKSASHPSLSSAGHS
 BnARF2: VRKIFLYIKKEEVKQNNPGTILSRSEEEAGVCEGSDAKDKSASHPSLSSAGHS
 OsARF2: VRKIFLYIKKEEVKQNNPGTILSRSEEEAGVCEGSDAKDKSASHPSLSSAGHS

SEQ ID
NO: 3SEQ ID
NO: 10SEQ ID
NO: 61